

## REMARKS

### **I. Status of the Claims**

Claims 1-30 are pending in the application, and claims 1-12, 23 and 28 stand withdrawn pursuant to a restriction requirement. Claims 13-22, 24-27, 29 and 30 have been examined and stand rejected, variously, under 35 U.S.C. §§101, 102 and 112 (first and second paragraphs). The specific grounds for rejection, and applicants' response thereto, are set out in detail below.

### **II. Traversal of the Restriction**

Applicants previously traversed the restriction requirement in that limitation to SEQ ID NO:4 was not believed proper given the high degree of homology between SEQ ID NO:2 and SEQ ID NO:4. The examiner's response was that no information was provided on this point. Applicants are attaching to this response a comparison of the two sequences, showing a 100% sequence homology with respect to the coding regions. Reconsideration and withdrawal of the restriction, as it applies to the issue of SEQ ID NOS:2 and 4, is therefore again respectfully requested.

### **III. Objections to the Specification and Claims**

The specification is objected to for a misspelling on page 12. An amendment has been provided.

Claim 18 is objected to for misspellings. An amendment has been provided.

Claim 15 is objected to as allegedly failing to limit the claim from which it depends. Claim 13 is a method claim, and the examiner argues that since claim 15 lacks a method step, it cannot limit claim 13. Applicants traverse. Claim 15 limits the method of claim 13 by a

qualification on the nature of the integrated nucleic acid, fragment or homologue, namely, that is a ribozyme. This is a valid limitation of a preceding claim.

Claim 21 is objected to as allegedly failing to limit the claim from which it depends. The use of the term “stringent conditions” without recitation of what stringent conditions are is said to be no limiting. Applicants traverse, but the claim has been canceled, rendering the rejection moot. However, to the extent that the recitation of “stringent conditions” now appears in other claims, applicants submit that the specification defines this term (see page 4, lines 13-17). Thus, the objection is believed to be improper.

Claim 24 is objected as allegedly failing to limit the claim from which it depends. Applicants traverse, but have canceled the claim.

Reconsideration and withdrawal of the rejections is therefore respectfully requested.

#### **IV. Rejection Under 35 U.S.C. §101**

Claim 26 is rejected as failing to distinguish a product of nature. An amendment has been provided that is believed to address the examiner’s concerns. Reconsideration and withdrawal of the rejection is therefore respectfully requested.

#### **V. Rejections Under 35 U.S.C. §112**

##### **A. First Paragraph**

Claims 13-18, 20-22, 24-27, 29 and 30 stand rejected as allegedly lacking an adequate written description under §112, first paragraph. The examiner argues that, under *Eli Lilly*, the failure of applicants to cite further nucleic acid sequences homologous to SEQ ID NO:4,

derivatives of SEQ ID NO:4, or sequences that hybridize to SEQ ID NO:4 having a specific biologic activity, renders the specification defective. Applicants traverse.

Applicants have amended the independent claims to recite either SEQ ID NO:4, fragments of that sequence, and/or homologues that hybridize to SEQ ID NO:4 under stringent conditions. For the first two, structural limitations of SEQ ID NO:4 are present and should avoid any written description concerns. As for homologues, it is routine practice for the PTO to grant claims to nucleic acid sequences that are defined by their degree of homology to a reference sequence, and to do so in the absence of specific examples. This can be done by stating the percent homology, or by defining that operational hybridization under certain conditions – in this case, stringent conditions. The *Eli Lilly* decision in no way has abrogated this practice.

Indeed, applicants' specification provides a great deal of information about what homologous sequences are:

The term "homologous sequence" or "homologous nucleic acid sequence" or "homologue" as used herein refers to a nucleic acid or protein sequence with significant similarity to the compared sequence or parts thereof, whereby this homologous sequences show an activity or part-activity comparable to the activity of the nucleic acid sequence or protein sequences according to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 or SEQ ID NO:4. As homologous sequences are considered nucleic acid sequences, which hybridize with the sequences according to SEQ ID NO:1, SEQ ID NO:2 or SEQ ID NO:4 or parts of these sequences under stringent or less stringent conditions (about stringent and less stringent conditions see Sambrook et al., Molecular Cloning, Cold Spring Harbour Laboratory (1989), ISBN 0-87969-309-6). An example for stringent hybridization condition is: hybridization in 4 x SSC at 65° C (alternatively in 50% formamide and 4 X SSC at 42° C), followed by several washing steps in 0,1 x SSC at 65°C for one hour. An example for less stringent hybridization condition is hybridization in 4 x SSC at 37° C, followed by several washing steps in 1 x SSC at room temperature. As homologous sequences are furthermore considered nucleic acid or protein sequences or parts thereof, which show a significant similarity with the nucleic acid and amino acid sequences of the present invention using the similarity algorithm BLAST (Basic Local Alignment Search Tool, Altschul et al., Journal of Molecular Biology 215, 403-410 (1990). As significant similar, as used herein, are considered sequences, which e.g. using standard

parameters in Blast-Service of NCBI show a Probability of  $P < 10^{-5}$ , if they are compared with the sequences according to SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 or SEQ ID NO:4 or parts thereof.

When one couples this information with SEQ ID NO:4 and the presently recited stringent hybridization conditions, one of ordinary skill in the art can easily envision a genus of nucleic acids that are very similar in structure to SEQ ID NO:4. Moreover, for several of the applications of these nucleic acids – ribozymes and antisense molecules – hybridization to SEQ ID NO:4 is the specified activity of import. This showing indeed satisfies the “second prong” of the *Eli Lilly* test, namely, “a recitation of structural features common to the genus ....” Thus, defined in this fashion, the claims as presented for reconsideration adequately reflect the invention which applicants possessed at the time of filing. Reconsideration and withdrawal of the rejection is therefore respectfully requested.

#### **B. Second Paragraph**

Claims 13-18, 21, 29 and 30 are rejected as allegedly indefinite. Claim 13 is rejected as implying that a nucleic acid has the activity of a polypeptide. Applicants have dropped the recitation in question from the claim.

Claim 13 is also rejected for use of the term “modified.” Applicants traverse, but in the interest of advancing the prosecution, the term has been dropped from the claim.

Claim 15 is rejected for alleged lack of antecedent basis for “the formation of flavonoids.” Applicants traverse, but in the interest of advancing the prosecution, the term has been dropped from the claim.

Claim 15 is also rejected as allegedly omitting steps which would inhibit the formation of flavonoids. Applicants traverse in that claim 13, from which claim 15, depends, provides the

step of stably integrating a nucleic acid sequence, fragment or homologue of SEQ ID NO:4, and claim 15 clarifies that the nucleic acid sequence, fragment or homologue further encodes a ribozyme. Thus, the claim does not omit any necessary step.

Claim 21 is rejected for the recitation of “stringent conditions.” As discussed above, to the specification adequately defines this term (see page 4, lines 13-17). Thus, the rejection is believed to be improper.

Reconsideration and withdrawal of all the preceding rejections is thus respectfully requested.

## **VI. Rejections Under 35 U.S.C. §102**

### **A. WO 99/00501**

Claims 13-18, 20-22, 24-27, 29 and 30 stand rejected under §102(b) as allegedly anticipated by the ‘501 application. Applicants traverse.

WO 99/00501 discloses nucleic acids encoding *TTG1* from *Arabidopsis*, which is believed to act in the pathways leading, *inter alia*, to trichome differentiation. This is distinct from the functions from *TT1*, which is involved in flavonoid biosynthesis in the seed coat only. Moreover, ‘501 does not disclose SEQ ID NO:4, nor has the examiner made any attempt to illustrate why the nucleic acid sequence of the *TTG1* gene of the ‘501 application would be believed to hybridize with SEQ ID NO:4 under *any* conditions, much less the stringent conditions now recited in the claims. Indeed, an amino acid comparison of TT1 (Accession No. AAL66406) and TTG1 (Accession No. CAC10524) using Blast2Sequences at NCBI shows a 0% match. As such, the examiner has failed to establish the lack of novelty of the claimed sequences. Reconsideration and withdrawal of the rejection is therefore respectfully requested.

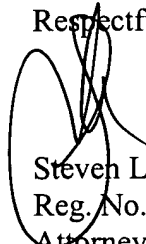
**B. Shirley *et al.* in view of Sagasser *et al.***

Claim 19 stands rejected under §102(b) as allegedly anticipated by Shirley *et al.*, in view of Sagasser *et al.* Applicants traverse, but in the interest of advancing the prosecution, the claim has been amended to recite that the nucleic acid is isolated and purified. Reconsideration and withdrawal of the rejection is therefore respectfully requested.

**VII. Conclusion**

In light of the foregoing, applicants submit that all claims are in condition for allowance, and an early notification to that effect is earnestly solicited. Should the examiner have any questions or comments regarding this application, a telephone call to the undersigned is invited.

Respectfully submitted,



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